AMENDMENTS

In the Specification:

Please replace paragraph [0067] on page 17 with the following paragraph:

[0067] Figure 3 is a graphic representation illustrating that Dam regulates in vivo induced genes. β-galactosidase expression from S. typhimurium ivi fusions in Dam⁺ and Dam⁻ strains grown in LB. The vertical axis shows β-galactosidase activities (μ-moles of o-nitrophenol (ONP) formed per minute per A_{600} unit per milliliter of cell suspension x 10^3).

Please replace paragraph [0068] on page 18 with the following paragraph:



[0068] Figure 4 is a graphic representation illustrating that Dam represses PhoP activated genes. β-galactosidase expression from S. typhimurium ivi fusions grown in minimal medium. The vertical axis shows β-galactosidase activities (μ-moles of o-nitrophenol (ONP) formed per minute per A_{600} unit per milliliter of cell suspension x 10^3). The dam genotype is shown below the horizontal axis, and the phoP genotype is shown as black (PhoP⁺) and gray (PhoP⁻) boxes.

Please replace paragraph [00244] on pages 67-68 with the following paragraph:

[00244] All bacterial strains used in this study were derivatives of S. typhimurium 14028 (strain 1). Mutant strains were isogenic to wild type and were obtained or constructed as described (Dam102::Mud-Cm and mutS121::Tn10 alleles are in LT2 (strain 7), a highly attenuated (virtually non-pathogenic) strain as shown in Table 2, were obtained from Dr. John Roth (University of Utah) and Dr. Tom Cebula (The Food and Drug Administration), respectively; these alleles (and additional alleles below) were transduced into virulent strain, 14028, constructing strains 2 and 5, respectively. Dam∆232 (strain 3) was constructed using

internal oligonucleotides that serve as PCR primers designed to construct an in-frame 300 bp deletion of defined *Dam* sequence. *dcm1*::Km was constructed according to (Julio, S. M., *et al.*, *Molec. Gen. Genet.*, **258**: 178-181 (1998)); the Km resistance determinant is associated with an internal deletion of > 600 bp of *dcm* sequence. The *lrp31*::Km is a null insertion in the *lrp* gene (strain 6). The Dam overproducing strain (strain 4) contains *E. coli Dam* on a recombinant plasmid (pTP166) in a wild-type background (Marinus, *et al.*, *Gene*, **28**:123-125 (1984).



Please replace TABLE 1 on page 70 with the following TABLE 1:

TABLE 1

Strain	Genotype	Oral LD ₅₀	I.P. LD ₅₀	Competitive Index (I.P.)
1	"wild type"	>10 ⁺⁵	<10	
2	Dam102::Mud-Cm	>10+9	>10 ⁺⁴	<10 ⁻⁴
3	Dam∆232 (non-polar deletion)	>10+9	>10 ⁺⁴	<10 ⁻⁴
4	wild type, (pTP166) (Dam overproducer)	10+8	>10 ⁺⁴	<10 ⁻⁴
5	mutS121::Tn10	10 ⁺⁵	ND	0.9
6	lrp31::Km	10 ⁺⁵	ND	10.0
7	LT2	ND	2 x 10 ⁺⁴	, ND



In the Claims:

Please cancel claim 5, add new claims 30 and 31 and amend claims 1, 3, 4, 7, and 18 to read as below:



1. (Amended) An immunogenic composition, comprising:

a pharmaceutically acceptable excipient; and